

URQUP16_seq.txt
SEQUENCE LISTING

<110> Sanders, Jane
Furmaniak, Jadwiga
Smith, Bernard Rees

<120> Binding Partners for the Thyrotropin Receptor and uses thereof

<130> URQU.P-016

<140> US 10/537,260
<141> 2003-11-28

<150> PCT/GB2003/005171
<151> 2003-11-28

<150> GB 0227964.4
<151> 2002-11-29

<150> GB 0302140.9
<151> 2003-01-29

<150> GB 0315147.9
<151> 2003-06-27

<160> 38

<170> PatentIn version 3.1

<210> 1
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Gln val Gln Leu val Gln Ser Gly Ala Glu val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Arg Gly Ser Gly Tyr Arg Phe Thr Ser Tyr
20 25 30

Trp Ile Asn Trp val Arg Gln Leu Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Thr Asp Ser Tyr Thr Asn Tyr Ser Pro Ser Phe
50 55 60

Lys Gly His val Thr val Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Gly Met Tyr Tyr Cys
85 90 95

Ala Arg Leu Glu Pro Gly Tyr Ser Ser Thr Trp Ser val Asn Trp Gly
100 105 110

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1 5 10 15

Gly

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Arg Gly Ser Gly Tyr Arg Phe Thr Ser Tyr
20 25 30

Trp Ile Asn Trp Val Arg Gln Leu Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Thr Asp Ser Tyr Thr Asn Tyr Ser Pro Ser Phe
50 55 60

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Lys Gly His Val Thr Val Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Gly Met Tyr Tyr Cys
85 90 95

Ala Arg Leu Glu Pro Gly Tyr Ser Ser Thr Trp Ser Val Asn Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
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Val Phe Pro
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Arg Val Thr Ile Ser Cys Ser Gly Asn Ser Ser Asn Ile Gly Asn Asn
20 25 30

Ala Val Asn Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Tyr Asp Asp Gln Leu Pro Ser Gly Val Ser Asp Arg Phe Ser
50 55 60

Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Thr Ser Trp Asp Asp Ser Leu
85 90 95

Asp Ser Gln Leu Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly
100 105 110

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<210> 8
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Tyr Asp Asp Gln Leu Pro Ser
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cccgggaaag gcctagagtg gatgggcagg attgatccta ctgactctta taccaactac 180
agtcctatcct tcaaaggcca cgtcaccgtc tcagctgaca agtccatcaa cactgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accggcatgt attactgtgc gaggctcgaa 300
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 cccgggaaag gcctagagtg gatgggcagg attgatccta ctgactctta taccaactac 180
 agtccatcct tcaaaggcca cgtcaccgtc tcagctgaca agtccatcaa cactgcctac 240
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 ccaggaaagg ctccaaact cctcatttat tatgatgatc aactgccctc aggggtctct 180
 gaccgattct ctggctccag gtctggcacc tccgcctccc tggccatccg tgggctccag 240
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<400> 16
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<210> 17
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<400> 18
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<210> 19
<211> 119
<212> PRT
<213> Mus sp.

<400> 19
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1 5 10 15
Ser Val Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30
Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ser Arg Asn Tyr Gly Ser Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Leu Thr Val Ser Ser
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<213> Mus sp.

<400> 20
Thr Tyr Trp Met His
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<210> 21

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<211> 17
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Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 22
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Asn Tyr Gly Ser Gly Tyr Tyr Phe Asp Tyr
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<210> 23
<211> 124
<212> PRT
<213> Mus sp.

<400> 23

Asp Val Gln Ile Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ser Arg Asn Tyr Gly Ser Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro
115 120

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Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Thr Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Trp Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 25
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<400> 25

Ser Ala Ser Ser Ser Val Ser Tyr Met His
 1 5 10

<210> 26
 <211> 7
 <212> PRT
 <213> Mus sp.

<400> 26

Asp Thr Ser Lys Leu Ala Ser
 1 5

<210> 27
 <211> 9
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 <213> Mus sp.

<400> 27

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<210> 28
<211> 110
<212> PRT
<213> Mus sp.

<400> 28

Gly Val Glu Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Thr Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Trp Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Leu Met Leu
100 105 110

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<400> 29

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cctggacaag gccttgagtg gatcggagag attgatcctt ctgatagtta tactaactat	180
aatcaaaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac	240
atgcacctca gcagcctgac atctgaggac tctgcggtct attactgttc aagaaactac	300
ggtagtggct actactttga ctactggggc caaggcacca ctctcacagt ctcctca	357

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<400> 30

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<210> 31
 <211> 51
 <212> DNA
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<400> 31
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51

<210> 32
 <211> 30
 <212> DNA
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<400> 32
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<210> 33
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 <212> DNA
 <213> Mus sp.

<400> 33
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 cctggacaag gccttgagtg gatcggagag attgatcctt ctgatagtta tactaactat 180
 aatcaaaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac 240
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 aaaacaacac ccc 373

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 acctcccca aaagatggat ttatgacaca tccaaactgg cttctggagt ccctgctcgc 180
 ttcagtggca gtgggtcttg gacctcttac tctctcacia tcagcagcat ggagactgaa 240
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<213> Mus sp.

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<400> 36
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<210> 37
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<400> 37
cagcagtggg gtagtaaccc gtggacg 27

<210> 38
<211> 331
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acctcccca aaagatggat ttatgacaca tccaaactgg cttctggagt ccctgctcgc 180
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accaaactgg aaatcaaacg gctgatgctg c 331